In the Specification:

Please replace the paragraph beginning at page 17, line 6, with the following:

--Figure 2 displays the nucleotide sequence (SEQ ID NO:2) of genomic DNA comprising the G564 coding sequence (amino acid sequence = SEQ ID NO:3) and promoter region from Scarlet Runner Bean (*Phaseolus coccineus*). The ATG start codon is displayed in bold and underlined nucleotides indicates intron sequences.--

Please replace the paragraph beginning at page 17, line 10, with the following:

--Figure 3 displays the nucleotide sequence (SEQ ID NO:4) of genomic DNA comprising the G564 coding sequence (amino acid sequence = SEQ ID NO:5) and promoter region from *Arabidopsis thaliana*. The ATG start codon is displayed in bold and underlined nucleotides indicates intron sequences.--

Please replace the paragraph beginning at page 17, line 13, with the following:

--Figure 4 displays the nucleotide sequence (SEQ ID NO:6) of genomic DNA comprising the C541 coding sequence (amino acid sequence = SEQ ID NO:7) and promoter region from Scarlet Runner Bean (*Phaseolus coccineus*). The ATG start codon is displayed in bold and underlined nucleotides indicates intron sequences.--

Please replace the paragraph beginning at page 17, line 17, with the following:

--Figure 5 displays the nucleotide sequence (SEQ ID NO:8) of genomic DNA comprising the C541 coding sequence (amino acid sequence = SEQ ID NO:9) and promoter region from *Arabidopsis thaliana*. The ATG start codon is displayed in bold and underlined nucleotides indicates intron sequences.--

Please replace the paragraph beginning at page 17, line 28, with the following:

B2

--Figure 8 identifies a number of promoter control elements (SEQ ID NOS:15-24) found within sequences –921 to –662 of Figure 2 (SEQ ID NOS:13 and 14) Figure 1.--

Please replace the paragraph beginning at page 52, line 13, with the following:

B3

--A cDNA library of 5-9 DAP Scarlet Runner Bean seeds containing globular-stage embryos was constructed using the ZAP Express® cDNA synthesis kit (Stratagene: La Jolla, CA). Poly(A) mRNA was used as a template to generate first-strand cDNA using MMLV reverse transcriptase and a 50-base oligonucleotide linker-primer [5'-$(GA)_{10}$ACTAGTCTCGAG$(T)_{18}$ -3' (SEQ ID NO:25)]. Double-strand cDNAs were blunt-ended and ligated to an EcoRI adapter. After phosphorylation of EcoRI 5' ends, the cDNAs were digested with XhoI and size-fractionated on a Sephacryl S-400 column to exclude cDNAs that were smaller than 250 bp. The fractionated cDNAs were ligated to the λZAP vector. About 3,000 recombinants from the unamplified library were differentially screened with ^{32}P-labeled first-strand cDNAs generated from: (1) 5-9 DAP seed micropylar region poly(A) mRNA and (2) leaf poly(A) mRNA. cDNA clones representing mRNAs preferentially present in the micropylar region were screened two more times following the strategy used in the primary screen.--

Please replace the paragraph beginning at page 52, line 27, with the following:

B4

--Differential display procedures of Liang and Pardee (Liang, P., *et al.*, *Science*, 257:967-971 (1992)) were followed using the RNAimage™ kit (GenHunter Corp.: Nashville, TN). Differential display reactions were carried out using total RNA templates from: (1) 6-8 DAP dissected suspensors of globular-stage embryos, (2) 6 DAY embryo-containing micropylar seed regions, (3) 6 DAP non-embryo-containing chalazal

seed regions, (4) 6-8 DAP isolated globular-stage embryo propers, (5) leaves, (6) ovules, (7) 2 DAY whole seeds, and (8) 3 DAP whole seeds. Briefly, first-strand cDNAs were generated by reverse transcription (RT) of 200 ng of total RNA using MMLV reverse transcriptase and an anchor/reverse primer (G primer: 5'-AAGCT$_{11}$G-3' (SEQ ID NO:26) or C primer: 5'-AAGCT$_{11}$C-3' (SEQ ID NO:27)). Aliquots of the first-strand cDNAs were used as templates for the polymerase chain reaction (PCR) using combinations of forward and anchor/reverse primers in the presence of ^{33}P-dCTP and AmpliTaq® polymerase (Perkin Elmer; Branchburg, NJ). The forward primers used were: H-AP49, 5'-AAGCTTTAGTCCA-3' (SEQ ID NO:28); H-AP50, 5'-AAGCTTTGAGACT-3' (SEQ ID NO:29); H-AP51, 5'-AAGCTTCGAAATG-3' (SEQ ID NO:30); H-AP52, 5'-AAGCTTGACCTTT-3' (SEQ ID NO:31); H-AP53, 5'-AAGCTTCCTCTAT-3' (SEQ ID NO:32); H-AP54, 5'-AAGCTTTTGAGGT-3' (SEQ ID NO:33); H-AP55, 5'-AAGCTTACGTTAG-3' (SEQ ID NO:34); and H-AP56, 5'-AAGCTTATGAAGG-3' (SEQ ID NO:35), where H-AP refers to the primers supplied by the RNAimage™ kit. The RT-PCR products were size-fractionated in a 6% acrylamide gel and visualized by autoradiography.

Please replace the paragraph beginning at page 53, line 23, with the following:

For pre-screening of differential display cDNA clones, PCR-amplifled cDNAs from different mRNA populations were generated following the procedures of Kelly *et al.* (1990), with minor modifications. Suspensor (6 DAP), ovule, 2 DAP seed, 3 DAP seed, 6 DAP micropylar region, 6 DAP chalazal region, and leaf total RNAs were isolated. First-strand cDNA was generated from 5 μg of each RNA using MMLV reverse transcriptase and 50 ng/μl of oligo(dT$_{20}$) (SEQ ID NO:36) as primer. The first-strand cDNAs were 3' tailed with poly(dA) using terminal transferase. PCR amplifications were carried out using tailed first-strand cDNAs as templates and 2 μM of dT$_{20}$dN (SEQ ID NO:37) (where dN = dG, dC, dA, or dT) as primer in 100 μl containing 20 mM Tris

(pH 8.4), 50 mM KCl, 1 mM $MgCl_2$, and 0.2 μM dNTPs at 94°C/1 minute, 42°C/2 minutes, and 72°C/5 minutes for 30 cycles, followed by a 10 minute extension at 72°C. A 1 μl aliquot from each reaction was used to perform another round of amplification using the same conditions. The reactions were extracted with phenol/chloroform and precipitated in ethanol. An aliquot equivalent to 1 μg from each reaction was size-fractionated in a 1% agarose gel, which was then used for DNA gel blot analysis according to the procedures of Sambrook *et al.*, *supra*.--

Please replace the paragraph beginning at page 55, line 28, with the following:

--The region surrounding the ATG start codon in *G564*g7.2.79 was converted into an SphI endonuclease restriction site by PCR using a T3 primer and a mutagenic oligo (5'-ATTGGACTGCATGCTTACGCTAGTCTGTGCAGAG-3'; SEQ ID NO:38). A 4.2 kb *G564* promoter region was cloned in the SphI site upstream of the *E coli β-Glucoronidase* (*GUS*) gene coding region (Jefferson, R. A., *et al.*, *EMBO. J.*, 6(13):3901-3907 (1987)) in pGEM5*GUS*. After cloning, the *G564* promoter region was re-sequenced. pGEMS*GUS* was constructed by inserting the *GUS* coding region and the Ti-plasmid *gene 7* 3' end from *TPI2/GUS* gene (Drews, G. N., *et al.*, *Plant Cell*, 4:1383-1404 (1992)) into the NcoI/NotI sites of pGEM5 (Promega: Madison, WI). The *G564/GUS* gene was transferred to the pHYGA (Hygromycin^R) plant transformation vector (Klucher, K. M., *et al.*, *Plant Cell*, 8:137-153 (1996)). Tobacco plants were transformed and regenerated using the leaf disk procedure of Horsch *et al.* (Horsch, *et al.*, *Science*, 227:1229-1231 (1985)).--

Please replace the paragraph beginning at page 63, line 13, with the following:

--A comparison of the Scarlet Runner Bean G564 promoter (SEQ ID NO:1) and the Scarlet Runner Bean C541 promoter identified a conserved 10 base pair sequence which may confer suspensor-specific activity. Supporting this assertion, the